

In the Specification:

The paragraph, beginning at page 2, line 34 has been amended as follows:

C¹ Purification and sequence analysis of the EGF-like domain has revealed the presence of six conserved cysteine residues which cross-bind to create three peptide loops, Savage *et al.*, *J. Biol. Chem.* 248: 7669-7672 (1979). It is now generally known that several other peptides can react with the EGF receptor which share the same generalized motif ~~$X_nCX_7CX_{4/5}CX_{10}CXCX_5GX_2CX_n$, where X represents any non-cysteine amino acid, and n is a variable repeat number.~~ Non isolated peptides having this motif include TGF- α , amphiregulin, schwannoma-derived growth factor (SDGF), heparin-binding EGF-like growth factors and certain virally encoded peptides (e.g., Vaccinia virus, Reisner, *Nature* 313: 801-803 (1985), Shope fibroma virus, Chang et al., *Mol Cell Biol.* 7: 535-540 (1987), Molluscum contagiosum, Porter and Archard, *J. Gen. Virol.* 68: 673-682 (1987), and Myxoma virus, Upton *et al.*, *J. Virol.* 61: 1271-1275 (1987), Prigent and Lemoine, *Prog. Growth Factor Res.* 4: 1-24 (1992).--

The paragraph, beginning at page 14, line 14, has been amended as follows:

C² Purification and sequence analysis of the EGF-like domain has revealed the presence of six conserved cysteine residues which cross-bind to create three peptide loops, Savage *et al.*, *J. Biol. Chem.* 248: 7669-7672 (1979). It is now generally known that several other peptides can react with the EGF receptor which share the same generalized motif $X_nCX_7CX_{4/5}CX_{10}CXCX_5GX_2CX_n$ (SEQ ID NO: 424), where X represents any non-cysteine amino acid, and n is a variable repeat number. Non isolated peptides having this motif include TGF- α , amphiregulin, schwannoma-derived growth factor (SDGF), heparin-binding EGF-like growth factors and certain virally encoded peptides (e.g., Vaccinia virus, Reisner AH, *Nature* 313: 801-803 (1985), Shope fibroma virus, Chang W., et al., *Mol Cell Biol.* 7: 535-540 (1987), Molluscum contagiosum, Porter CD & Archard LC, *J. Gen. Virol.* 68: 673-682 (1987), and Myxoma virus, Upton C *et al.*, *J. Virol.* 61: 1271-1275 (1987). Prigent SA & Lemoine N.R., *Prog. Growth Factor Res.* 4: 1-24 (1992).--

The paragraph, beginning at page 69, line 6, has been amended as follows:

C3
Percent amino acid sequence identity may also be determined using the sequence comparison program NCBI-BLAST2 (Altschul et al., Nucleic Acids Res. 25:3389-3402 (1997)).
The ~~NCBI-BLAST2 sequence comparison program may be downloaded from~~ <http://www.ncbi.nlm.nih.gov>. NCBI-BLAST2 uses several search parameters, wherein all of those search parameters are set to default values including, for example, unmask = yes, strand = all, expected occurrences = 10, minimum low complexity length = 15/5, multi-pass e-value = 0.01, constant for multi-pass = 25, dropoff for final gapped alignment = 25 and scoring matrix = BLOSUM62.

The paragraph, beginning at page 71, line 26, has been amended as follows:

C4
Percent nucleic acid sequence identity may also be determined using the sequence comparison program NCBI-BLAST2 (Altschul et al., Nucleic Acids Res. 25:3389-3402 (1997)).
The ~~NCBI-BLAST2 sequence comparison program may be downloaded from~~ <http://www.ncbi.nlm.nih.gov>. NCBI-BLAST2 uses several search parameters, wherein all of those search parameters are set to default values including, for example, unmask = yes, strand = all, expected occurrences = 10, minimum low complexity length = 15/5, multi-pass e-value = 0.01, constant for multi-pass = 25, dropoff for final gapped alignment = 25 and scoring matrix = BLOSUM62.

The paragraph beginning at page 147, line 27, has been amended as follows:

C5
The extracellular domain (ECD) sequences (including the secretion signal sequence, if any) from about 950 known secreted proteins from the Swiss-Prot public database were used to search EST databases. The EST databases included public databases (e.g., Dayhoff, GenBank), and proprietary databases (e.g. LIFESEQ™, Incyte Pharmaceuticals, Palo Alto, CA). The search was performed using the computer program BLAST or BLAST2 (Altschul, and Gish, Methods in Enzymology 266: 460-80 (1996); <http://blast.wustl.edu/blast/README.html>) as a comparison of the ECD protein sequences to a 6 frame translation of the EST sequences. Those comparisons with a Blast score of 70 (or in some cases 90) or greater that did not encode known proteins were

clustered and assembled into consensus DNA sequences with the program "phrap" (Phil Green, University of Washington, Seattle, Washington).

The paragraph, beginning at page 154, line 14 has been amended as follows:

C6 -The EST sequence accession number AF007268, a murine fibroblast growth factor (FGF-15) was used to search various public EST databases (e.g., GenBank, Dayhoff, etc.) The search was performed using the computer program BLAST or BLAST2 Altschul et al., Methods in Enzymology, 266:460-480 (1996); <http://blast.wustl.edu/blast/README.html> as a comparison of the ECD protein sequences to a 6 frame translation of the EST sequences. The search resulted in a hit with GenBank EST AA220994, which has been identified as stratagene NT2 neuronal precursor 937230.

The paragraph beginning at page 167, line 30, has been amended as follows:

C7 -The extracellular domain (ECD) sequences (including the secretion signal, if any) of from about 950 known secreted proteins from the Swiss-Prot public protein database were used to search expressed sequence tag (EST) databases. The EST databases included public EST databases (e.g., GenBank) and a proprietary EST DNA database (LIFESEQ™, Incyte Pharmaceuticals, Palo Alto, CA). The search was performed using the computer program BLAST or BLAST2 (Altschul et al., Methods in Enzymology 266:460-480 (1996)) as a comparison of the ECD protein sequences to a 6 frame translation of the EST sequence. Those comparisons resulting in a BLAST score of 70 (or in some cases 90) or greater that did not encode known proteins were clustered and assembled into consensus DNA sequences with the program "phrap" (Phil Green, University of Washington, Seattle, Washington; <http://bozeman.mbt.washington.edu/phrap.docs/phrap.html>).

The paragraph beginning at page 178, line 14, has been amended as follows:

C8 -The extracellular domain (ECD) sequences (including the secretion signal, if any) of from about 950 known secreted proteins from the Swiss-Prot public protein database were used to search expressed sequence tag (EST) databases. The EST databases included public EST

C8
databases (e.g., GenBank) and a proprietary EST DNA database (LIFESEQ™, Incyte Pharmaceuticals, Palo Alto, CA). The search was performed using the computer program BLAST or BLAST2 (Altshul et al., Methods in Enzymology 266:460-480 (1996)) as a comparison of the ECD protein sequences to a 6 frame translation of the EST sequence. Those comparisons resulting in a BLAST score of 70 (or in some cases 90) or greater that did not encode known proteins were clustered and assembled into consensus DNA sequences with the program "phrap" (Phil Green, University of Washington, Seattle, Washington; <http://bozeman.mbt.washington.edu/phrap.docs/phrap.html>).--
